S1-22

ORIGIN OF 2N GAMETES IN C. RETICULATA CV FORTUNE MANDARIN

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Citrus are most important fruit crop worldwide. Seedlessness is a key characteristic for the fresh fruit market and the development of triploid hybrids is one strategy developed by several groups over the world. Indeed, triploid hybrids are generally sterile and produce seedless fruits and do not pollinate other varieties. Triploid citrus hybrids can be obtained by several strategies, including hybridization between diploid parents.

Mechanism of 2n gamete formation and its implication on parental heterozygosity restitution is a main parameter determining the genetic and phenotypic structure of the triploid population. In the case of Citrus it has been shown that the 2n gametes are of maternal origin. It has been proposed that the origin of 2n gametes is from the second division restitution (SDR) in Clementines and from the first division restitution (FDR) in sweet oranges. No data is available for other genotypes and particularly 'Fortune', a mandarin hybrid producing very high rate of triploids in 2x x 2x crosses and massively used to create triploid progenies. The aim of this work was to analyse the mechanism of 2n gamete formation in 'Fortune' mandarin genotype.

One hundred and five triploid hybrids from the crosses between 'Fortune' as female diploid parent and 'Murcott' or 'Mandarino Común' as male diploid parents were genotyped for twenty-four codominant molecular SSRs (Simple Sequence Repeat) markers using a capillary genetic fragment analyzer. Estimation of allelic doses from relative peaks area allowed inferring the female and male gamete structures and thus the heterozygosity restitution in the 2n gametes.; this demonstrated that all triploid arise from 2n megaspores. The unimodal distribution of heterozygosity restitution in the 2n megaspores among the analyzed genotypes suggests that all these 2n gametes arise from a same mechanism. Restitution of maternal heterozygosity for the used markers makes suppose that underlying mechanism in the 2n gamete formation is SDR. Indeed there are six markers with less than 50% of maternal heterozygosity restitution, which is incompatible with FDR hypothesis. SDR hypothesis is coherent with the results published in case of the clementine, which is one of the parents of the 'Fortune' variety. Under this hypothesis, the relatively high global heterozygosity restitution level (60,95%) should indicate that a majority of the analyzed markers are far from the centromeres. This genetic structuration will soon be confronted with phenotypic variability and compared with structuration obtained with other triploid creation strategies such as 2x x 4x hybridization.

Keywords: citrus, mandarin, triploid, 2n gametes, meiosis

S04.022

Tetraploid *Citrus limonia* Rootstocks Are More Tolerant to Water Deficit than Parental Diploids and Present Large Gene Expression Changes in Roots

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Water shortage is one of the main abiotic constraints affecting growth and yield in citrus. In this work, we investigated the tolerance to water stress of diploid and tetraploid seedlings of Rangpur lime (*Citrus limonia*) and also their behaviour as rootstocks of Valencia Delta orange (*Citrus sinensis*) variety. The tetraploid (4*x*) line arose from chromosome doubling in nucellar cells of diploid (2*x*) Rangpur lime and has strictly the same allelic composition than the 2*x* one. At the beginning of the stress, leaf stomatal conductances of 4*x* seedlings and Valencia Delta orange grafted on 4*x* rootstocks were respectively lower than those of 2*x* seedlings and Valencia Delta orange grafted on 2*x* rootstocks. At the end of the experiment, 4*x* seedlings and Valencia Delta orange grafted on 4*x* showed the highest tolerances. This work suggests that greater tolerance is linked to a more efficient regulation of gas exchanges in 4*x* seedlings and varieties grown on 4*x* genotypes. Investigations of ABA root content in 2*x* and 4*x* suggest that constitutive biosynthesis of this hormone is higher in 4*x*. To have a better understanding of the impact of 2*x* and 4*x* rootstocks on scion, we have also investigated gene expression using 20 K cDNA microarrays and qRT-PCR in Valencia Delta leaves grafted on 2*x* and 4*x* rootstocks in control and water deficit conditions. Expression of candidate genes involved in water deficit tolerance was also monitored at the root level using qRT-PCR. In control condition, those different genes, including NCED1 which is involved in the last step of ABA biosynthesis, were all shown to be up regulated in 4*x* roots when compared to 2*x*.

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Distinctive Transcriptome Response of Two Strawberry (Fragaria xananassa) Cultivars to *Colletotrichum acutatum* Infection

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Strawberry (*Fragaria ×ananassa*) yields are strongly affected by fungal diseases and pests (i.e. *Colletotrichum* spp., are major pathogens of strawberry), forcing the excessive use of chemical products (mostly environmental contaminants) to control them. Resistant cultivars are a priority of most strawberry breeding programmes. However, little is known about the genetic basis that control strawberry resistance to pathogens, and totally resistant cultivars have not yet been reported. Although molecular markers of disease resistance in strawberry have been reported, the octoploid genetic structure of commercial strawberry makes it difficult to associate molecular markers with disease resistance genes. To gain insights into the genetic mechanisms of defense against *C. acutatum*, t
Camarosa and Andana) exhibitin
analyzed. An in-house cDNA m
was fabricated from a strawberry
obtained in response to this pat
cultivars was performed before a
was significantly altered (Pvalue=
(70 up-/24 down-regulated), anc
clusively alterated in Camarosa a
up-regulated in both cultivars. In
known gene of the public databa
function. Over-expression and si
analysis of candidate genes. Valua
effective control strategies to incre

S04.024

Expression Profiles o in Responses to Aph Chrysanthemum Cul

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In order to reveal how defense-relat
mum (*Chrysanthemum grandiflor*
0.5 h, 1 h, 3 h, 6 h, 12 h, 24 h, 3
expression profiles of genes involve
and flavonoids pathway including
phenylalanine ammonia lyase (PAL
late 5-hydroxylase (F5H), chalcone
(DFR) were determined using real-
tivars differing in aphid resistance.
COMT and F5H were induced in l
resistant cultivar 'Han6' and susce
were induced only in two aphid re
'Jinba' at any time point. The trans
genes increased more rapidly and pe
and 'Han6' than in the susceptible
genes reached their first peak at 1 h,
resistant cultivar 'Keiun', and peake
sistant cultivar 'Han6'. While in su
6 h, 3 d, 6 h, 12 h, respectively. The
to aphid inoculation were differen
suggesting that these genes probabl
chrysanthemum.

S04.025

Cloning of Genes Cor and Salt Tolerance by CDNA Library in Vege

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To obtain genes conferring allergenic
bean [*Glycine max* (L.) Merr.], a ful
seeds of the cultivar 'NN99-10' was
phoresis results showed that most of
2.0 kb, with an average size around 8
the recombination rate was above 99
library constructed was a full-length
selection followed by sequencing of th
library, a total of 642 expressed sequer